1600 1648

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RAW SEQUENCE LISTING DATE: 01/14/2002
PATENT APPLICATION: US/09/976,736 TIME: 18:44:34

Input Set : N:\Crf3\RULE60\09976736.raw
Output Set: N:\CRF3\01142002\I976736.raw

<110> APPLICANT: Bass, Michael B
Sullivan, John K
Theill, Lars E
Wang, Daguang
<120> TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
<130> FILE REFERENCE: A-548
<140> CURRENT APPLICATION NUMBER: US/09/976,736
<141> CURRENT FILING DATE: 2001-10-09
<150> PRIOR APPLICATION NUMBER: US/09/161,241
<151> PRIOR FILING DATE: 1998-09-25
<160> NUMBER OF SEQ ID NOS: 78
<170> SOFTWARE: PatentIn Ver. 2.0
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cctcaggagg aagctacgct caatgagatg tttcgagagg tggaggagct gatggaagac 180
actcagcaca aactgcgcag tgccgtggag gagatggagg cggaagaagc agctgctaaa 240
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gagaccaggg tgggaaataa cacagtccat gtgcaccagg aagttcacaa gataaccaac 360
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ttctccagct tcaagtacac ctgccagcca tgccgggacc agcagatgct atgcacccga 540
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tgccatgacc ccaccagcca gctgctggat ctcatcacct gggaactgga gcctgaagga 780
gctttggacc gatgcccctg cgccagtggc ctcctatgcc agccacacag ccacagtctg 840
gtgtacatgt gcaagccagc cttcgtgggc agccatgacc acagtgagga gagccagctg 900
cccagggagg ccccggatga gtacgaagat gttggcttca taggggaagt gcgccaggag 960
ctggaagacc tggagcggag cctagcccag gagatggcat ttgaggggcc tgcccctgtg 1020
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<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Human
<400> SEQUENCE: 2
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ccgcaggagg aggccaccct caatgagatg ttccgcgagg ttgaggaact gatggaggac 180
acgcagcaca aattgcgcag cgcggtggaa gagatggagg cagaagaagc tgctgctaaa 240
gcatcatcag aagtgaacct ggcaaactta cctcccagct atcacaatga gaccaacaca 300
gacacgaagg ttggaaataa taccatccat gtgcaccgag aaattcacaa gataaccaac 360
aaccagactg gacaaatggt cttttcagag acagttatca catctgtggg agacgaagaa 420

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ggcagaagga gccacgagtg catcatcgac gaggactgtg ggcccagcat gtactgccag 480
tttgccagct tccagtacac ctgccagcca tgccggggcc agaggatgct ctgcacccgg 540
gacagtgagt gctgtggaga ccagctgtgt gtctggggtc actgcaccaa aatggccacc 600
aggggcagca atgggaccat ctgtgacaac cagagggact gccagccggg gctgtgctgt 660
gccttccaga gaggcctgct gttccctgtg tgcacacccc tgcccgtgga gggcgagctt 720
tgccatgacc ccgccagccg gcttctggac ctcatcacct gggagctaga gcctgatgga 780
gccttggacc gatgcccttg tgccagtggc ctcctctgcc agccccacag ccacagcctg 840
gtgtatgtgt gcaagccgac cttcgtgggg agccgtgacc aagatgggga gatcctgctg 900
cccagagagg tccccgatga gtatgaagtt ggcagcttca tggaggaggt gcgccaggag 960
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<212> TYPE: DNA
<213> ORGANISM: Human
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gctatcaaga acctgccccc accgctgggc ggcgctgcgg ggcacccagg ctctgcagtc 180
agcgccgcgc cgggaatcct gtacccgggc gggaataagt accagaccat tgacaactac 240
cagccgtacc cgtgcgcaga ggacgaggag tgcggcactg atgagtactg cgctagtccc 300
acccgcggag gggacgcggg cgtgcaaatc tgtctcgcct gcaggaagcg ccgaaaacgc 360
tgcatgcgtc acgctatgtg ctgccccggg aattactgca aaaatggaat atgtgtgtct 420
tctgatcaaa atcatttccg aggagaaatt gaggaaacca tcactgaaag ctttggtaat 480
gatcatagca ccttggatgg gtattccaga agaaccacct tgtcttcaaa aatgtatcac 540
accaaaggac aagaaggttc tgtttgtctc cggtcatcag actgtgcctc aggattgtgt 600
tgtgctagac acttctggtc caagatctgt aaacctgtcc tgaaagaagg tcaagtgtgt 660
accaagcata ggagaaaagg ctctcatgga ctagaaatat tccagcgttg ttactgtgga 720
gaaggtctgt cttgccggat acagaaagat caccatcaag ccagtaattc ttctaggctt 780
cacacttgtc agagacacta a 801

<210> SEQ ID NO: 4
<211> LENGTH: 780
<212> TYPE: DNA
<213> ORGANISM: Mouse
<400> SEQUENCE: 4
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tctctaggag gggagactcc tgctcagtca gccaaccgat ctgcaggcat gaaccaagga 180
ctggctttcg gcggcagtaa gaagggcaaa agcctggggc aggcctaccc ttgcagcagt 240
gataaggaat gtgaagttgg aagatactgc cacagtcccc accaaggatc atcagcctgc 300
atgctctgta ggaggaaaaa gaaacgatgc cacagagatg ggatgtgttg ccctggtacc 360
cgctgcaata atggaatctg catcccagtc actgagagca tcctcacccc acatatccca 420
gctctggatg gcacccggca tagagatcgc aaccatggtc actattccaa ccatgacctg 480
ggatggcaga atctaggaag gccacactcc aagatgcctc atataaaagg acatgaagga 540
gacccatgcc tacggtcatc agactgcatt gatgggtttt gttgtgctcg ccacttctgg 600
accaaaatct gcaaaccagt gctccatcag ggggaagtct gtaccaaaca acgcaagaag 660
ggttcgcacg ggctggagat tttccagagg tgtgactgtg caaagggcct gtcctgcaaa 720
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<210> SEQ ID NO: 5

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Input Set : N:\Crf3\RULE60\09976736.raw
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105 <211> LENGTH: 780
106 <212> TYPE: DNA
107 <213> ORGANISM: Human
108 <400> SEQUENCE: 5
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110 ctgatggtgg agagctcaca gatcggcagt tcgcgggcca aactcaactc catcaagtcc 120
111 tctctgggcg gggagacgcc tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga 180
112 ctggcattcg gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 240
113 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc atcggcctgc 300
114 atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg gcatgtgctg ccccagtacc 360
115 cgctgcaata atggcatctg tatcccagtt actgaaagca tcttaacccc tcacatcccg 420
116 gctctggatg gtactcggca cagagatcga aaccacggtc attactcaaa ccatgacttg 480
117 ggatggcaga atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 540
118 gacccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg tcatttctgg 600
119 accaaaatct gcaaaccagt gctccatcag ggggaagtct gtaccaaaca acgcaagaag 660
120 ggttctcatg ggctggaaat tttccagcgt tgcgactgtg cgaagggcct gtcttgcaaa 720
121 gtatggaaag atgccaccta ctcctccaaa gccagactcc atgtgtgtca gaaaatttga 780
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124 <211> LENGTH: 624
125 <212> TYPE: DNA
126 <213> ORGANISM: Human
127 <400> SEQUENCE: 6
128 atggccgcgt tgatgcggag caaggattcg tcctgctgcc tgctcctact ggccgcggtg 60
129 ctgatggtgg agagctcaca gatcggcagt tcgcgggcca aactcaactc catcaagtcc 120
130 tctctgggcg gggagacgcc tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga 180
131 ctggcattcg gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 240
132 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc atcggcctgc 300
133 atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg gcatgtgctg ccccagtacc 360
134 cgctgcaata atgggcatga aggagacccc tgcctacgat catcagactg cattgaaggg 420
135 ttttgctgtg ctcgtcattt ctggaccaaa atctgcaaac cagtgctcca tcaggggaa 480
136 gtctgtacca aacaacgcaa gaagggttct catgggctgg aaatttcca gcgttgcgac 540
137 tgtgcgaagg gcctgtcttg caaagtatgg aaagatgcca cctactcctc caaagccaga 600
138 ctccatgtgt gtcagaaaat ttga 624
140 <210> SEQ ID NO: 7
141 <211> LENGTH: 675
142 <212> TYPE: DNA
143 <213> ORGANISM: Human
144 <400> SEQUENCE: 7
145 atggtggcgg ccgtcctgct ggggctgagc tggctctgct ctcccctggg agctctggtc 60
146 ctggacttca acaacatcag gagctctgct gacctgcatg gggcccggaa gggctcacag 120
147 tgcctgtctg acacggactg caataccaga aagttctgcc tccagccccg cgatgagaag 180
148 ccgttctgtg ctacatgtcg tgggttgcgg aggaggtgcc agcgagatgc catgtgctgc 240
149 cctgggacac tctgtgtgaa cgatgtttgt actacgatgg aagatgcaac cccaatatta 300
150 gaaaggcagc ttgatgagca agatggcaca catgcagaag gaacaactgg gcacccagtc 360
151 caggaaaacc aacccaaaag gaagccaagt attaagaaat cacaaggcag gaagggacaa 420
152 gagggagaaa gttgtctgag aacttttgac tgtggccctg gactttgctg tgctcgtcat 480
153 ttttggacga aaatttgtaa gccagtcctt ttggagggac aggtctgctc cagaagaggg 540
154 cataaagaca ctgctcaagc tccagaaatc ttccagcgtt gcgactgtgg ccctggacta 600
155 ctgtgtcgaa gccaattgac cagcaatcgg cagcatgctc gattaagagt atgccaaaaa 660

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Input Set : N:\Crf3\RULE60\09976736.raw
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atagaaaagc tataa 675

<210> SEQ ID NO: 8
<211> LENGTH: 349
<212> TYPE: PRT
<213> ORGANISM: Mouse
<400> SEQUENCE: 8

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            20                  25                  30
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
        35                  40                  45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50                  55                  60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65                  70                  75                  80
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
                85                  90                  95
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
            100                 105                 110
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
        115                 120                 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
    130                 135                 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
145                 150                 155                 160
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
                165                 170                 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
            180                 185                 190
Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
        195                 200                 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
    210                 215                 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225                 230                 235                 240
Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu
                245                 250                 255
Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
            260                 265                 270
Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe
        275                 280                 285
Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala
    290                 295                 300
Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu
305                 310                 315                 320
Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly
                325                 330                 335
Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
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209 <211> LENGTH: 350
210 <212> TYPE: PRT
211 <213> ORGANISM: Human
212 <400> SEQUENCE: 9
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215       Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
216                    20                  25                  30
217       Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
218                35                  40                  45
219       Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
220            50                  55                  60
221       Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
222        65                  70                  75                  80
223       Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
224                       85                  90                  95
225       Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
226                  100                 105                 110
227       Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
228              115                 120                 125
229       Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
230          130                 135                 140
231       His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
232       145                 150                 155                 160
233       Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
234                       165                 170                 175
235       Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
236                  180                 185                 190
237       Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
238              195                 200                 205
239       Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
240          210                 215                 220
241       Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
242       225                 230                 235                 240
243       Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
244                       245                 250                 255
245       Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
246                  260                 265                 270
247       Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
248              275                 280                 285
249       Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
250          290                 295                 300
251       Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
252       305                 310                 315                 320
253       Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
254                       325                 330                 335
255       Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
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L:450 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15